IN THE SPECIFICATION:

Page 1, delete the first seven (7) printed lines.

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IN THE CLAIMS:

Cancel claim 7, without prejudice or disclaimer of its subject matter.

Amend claims 1-6 as follows:

1. (amended) A method for [discriminating among] analyzing members of one or more taxonomic groups by hybridization [analysis] of operon subsequences either as DNA or as RNA product(s) comprising the steps of:

a. selecting an operon and determining operon subsequence hybridization reactivity by testing samples with [each] one or more oligonucleotide probes under controlled stringency conditions at two or more temperatures [relative to] at and above the probe's calculated or experimentally determined T_m or by making equivalent [other] changes in the hybridization solution,

b. contacting individually one or more samples that may contain operon subsequences with one or more oligonucleotide probes,

c. incubating the probes and samples at various temperatures and other conditions such that increasing degrees of stringency are obtained, and

d. assaying for hybridization of the probes to the samples in order to determine the relative level of reactivity of the combination of operon subsequences present in each sample.

2. (amended) The method of claim 1, wherein a probe of SEQ ID NO. 1 is used to analyze [for discriminating among] the genera Shigella and Escherichia and their species present in a sample, wherein [probe Seq. ID: Number] SEQ ID NO. 1 has the sequence CAG CTT GCT CTT CGC TGA CG [and is used].

3. (amended) The method of claim 1, wherein a probe of SEQ ID NO. 2 is used to analyze [for discriminating among] the genera Shigella and Escherichia and their species present in a sample, wherein [probe Seq. ID: Number] SEQ ID NO. 2 has the sequence AAA GCA GCT TGC TCT TTG CT [and is used].

4. (amended) The method of claim 1, wherein a probe of SEQ ID NO. 3 is used to analyze [for discriminating among] the genera Shigella and Escherichia and their species present in a sample, wherein [probe Seq. ID: Number] SEQ ID NO. 3 has the sequence CGA CGC AAC GCG AAG AAC TT [and is used].

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5. (amended) The method of claim 1, wherein a probe of SEQ ID NO. 4 is used to analyze [for discriminating among] the genera Shigella and Escherichia and their species present in a sample, wherein [probe Seq. ID: Number] SEQ ID NO. 4 has the sequence GAA GCT TGC TTC TTT GCT GAC [and is used].

6. (amended) RNA sequences for probes comprising a sequence selected from the group consisting of [Seq. ID: Numbers] SEQ ID NOs. 1, 2, 3, [or] and 4 wherein U substitutes for T.

Insert new claim 8.

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-- 8. A nucleic acid probe comprising the sequence of one of SEQ ID NO. 1-4 or variants thereof, capable of distinguishing between species of Shigella in a hybridization assay, or capable of distinguishing between Shigella and E. coli in a hybridization assay.--

IN THE ABSTRACT:

After the last page of the specification, **insert** the ABSTRACT appearing on the sheet accompanying this paper.

Remarks

Applicant requests reconsideration and timely notice of allowance of all the pending claims.

Applicant has amended claims 1-6 to address the PTOs concerns over indefiniteness. Claim 7 has been canceled and new claim 8 added. The amendments introduce no new matter.

An abstract has been added to the application on a separate sheet, as requested by the PTO.

Applicant notes that the Office Action refers to the results of a sequence search at page 6. However, applicant did not find these results in the material mailed. In order to discuss the results